

Proteomic Changes During Human Development: Defining the Cell Surface Proteome of Embryonic Stem Cells

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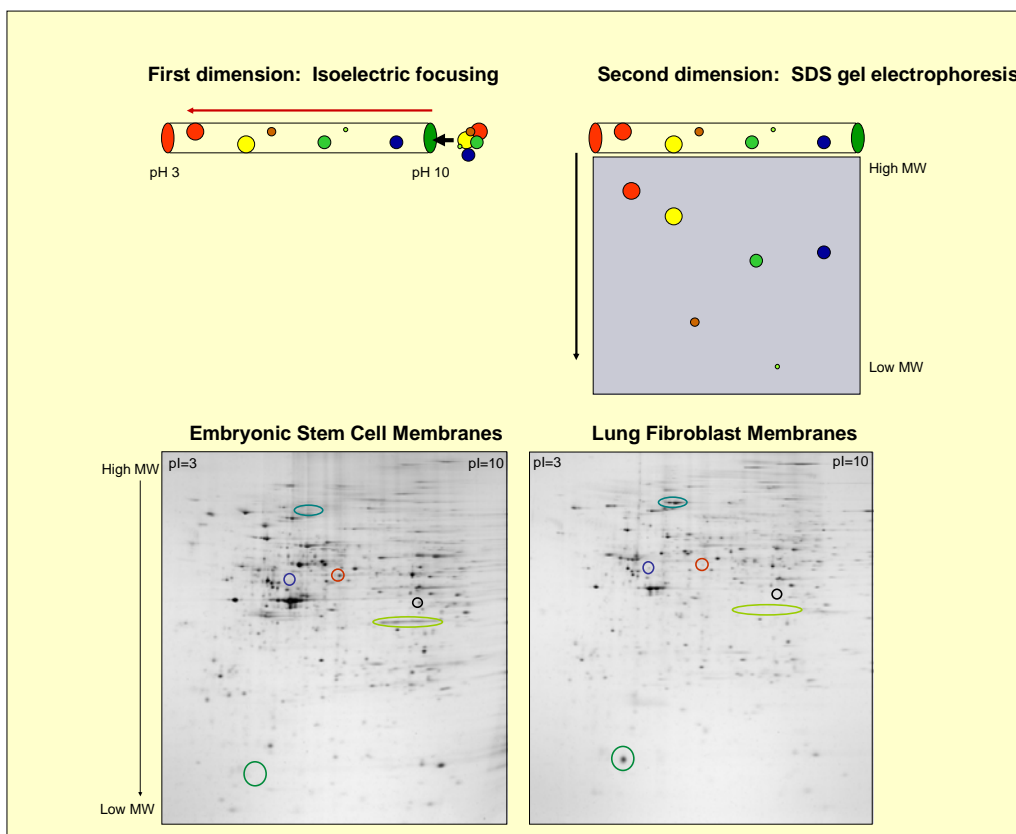
Embryonic stem cells have the capacity to become any cell type. We want to identify cell surface proteins that contribute to differentiation into neuronal cells.

Abstract

Within an animal, each cell has the same genetic content (DNA) but different functions and characteristics. What makes the cells of, for example, the liver and the brain look and function differently is the complement of proteins that are expressed in those cells, the proteome. We analyze membrane proteins from different types of human cells to look for differences in protein expression. This may provide a clue to the different behaviors of various cell types.

Methods

We use two-dimensional (2D) electrophoresis to visually analyze a cell's proteome. The first dimension of electrophoresis separates proteins based on their charge (isoelectric focusing). The second dimension separates proteins based on their size (SDS polyacrylamide gel electrophoresis). The proteins are then visualized by staining with silver and software is used to identify changes in protein expression. Proteins can be identified by mass spectroscopy of spots cut out of the gel.



Results and Conclusions

There are many membrane proteins present in both stem cells and lung fibroblasts. Most proteins appear in both cell types. Some proteins, whose identities are not known, appear to be expressed in stem cells or fibroblasts, but not both.

Goals for Future Work

We have two goals to further this work. First, we want to isolate and compare only the proteins that are on the cell surface. Secondly, we want to compare embryonic stem cells to neuronal stem cells to identify protein expression differences along this developmental pathway.

For More Information

For more about the Protein Mapping Group at Argonne National Laboratory, visit

proteomeweb.anl.gov

Acknowledgements

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